

CLAIMS

1. An agent for treating cancer which comprises as an active ingredient a polypeptide encoded by KIAA0172 gene, a partial sequence thereof or a variant thereof.
2. An agent for treating cancer which comprises as an active ingredient an oligonucleotide including KIAA0172 gene sequence, a part thereof or a variant thereof.
3. An agent for detecting cancer which comprises an antibody which recognizes a polypeptide encoded by KIAA0172 gene.
4. An agent for detecting cancer which comprises an oligonucleotide including KIAA0172 gene sequence, a part thereof or a variant thereof.
5. A composition for treating cancer which comprises the agent for treating cancer according to claim 1 or 2 and a pharmaceutically acceptable carrier.
6. A composition for detecting cancer which comprises the agent for detecting cancer according to claim 3 or 4 and a pharmaceutically acceptable carrier.
7. A vector for treating cancer which comprises KIAA0172 gene, a partial sequence thereof or a variant thereof.
8. A vector for detecting cancer which comprises KIAA0172 gene, a partial sequence thereof or a variant thereof.
9. A method for detecting cancer using an antibody which recognizes KIAA0172 protein.
10. The method for detecting cancer according to claim 9, which comprises a step of contacting a sample with an antibody which recognizes a polypeptide encoded by KIAA0172 gene.
11. The method for detecting cancer according to claim 9 or 10, wherein said method is immunostaining using a tissue section.
12. The method for detecting cancer, which comprises a step of contacting a sample with an oligonucleotide containing KIAA0172 gene sequence.
13. A modified KIAA0172 gene or a fragment thereof having at least one of the following mutations (a) to (h):

(a) Mutation from CAC to CAG at the 52nd codon

- (b) Mutation from GCG to GTG at the 168th codon
 - (c) Insertion of 6 nucleotides GCTGTA between the 268th and the 269th codons
 - (d) Mutation from GTA to GGA at the 269th codon
 - (e) Mutation from GAG to CAG at the 274th codon
 - (f) Mutation from TCC to GCC at the 306th codon
 - (g) Mutation from GCA to GTA at the 506th codon
 - (h) Mutation from CGT to CAT at the 509th codon.
14. An agent for detecting cancer which comprises the modified KIAA0172 gene according to claim 13.
15. The method for detecting cancer, which comprises a step of contacting a sample with an oligonucleotide containing the modified KIAA0172 gene sequence according to claim 13 or a part thereof.
16. A detecting method for evaluating the risk of suffering from cancer, which comprises a step of contacting a sample with an oligonucleotide containing the modified KIAA0172 gene sequence according to claim 13 or a part thereof.
17. A gene fragment containing at least one of the following single nucleotide polymorphism sites (i) to (r) on the KIAA0172 gene:
- (i) T/G polymorphism site for the third nucleotide of the codon number 273
 - (j) G/C polymorphism site for the third nucleotide of the codon number 299
 - (k) C/T polymorphism site for the first nucleotide of the codon number 372
 - (l) T/G polymorphism site for the third nucleotide of the codon number 380
 - (m) T/G polymorphism site for the third nucleotide of the codon number 497
 - (n) C/T polymorphism site for the third nucleotide of the codon number 453
 - (o) C/T polymorphism site for the third nucleotide of the codon number 478
 - (p) G/T polymorphism site for the third nucleotide of the codon number 507
 - (q) C/T polymorphism site for the third nucleotide of the codon number 1003 and
 - (r) G/C polymorphism site for the third nucleotide of the codon number 1120.

18. A method for evaluating the risk of suffering from cancer, which comprises determining the respective nucleotides at the following single nucleotide polymorphism sites (i) to (r) on the KIAA0172 gene:
- (i) T/G polymorphism site for the third nucleotide of the codon number 273
 - (j) G/C polymorphism site for the third nucleotide of the codon number 299
 - (k) C/T polymorphism site for the first nucleotide of the codon number 372
 - (l) T/G polymorphism site for the third nucleotide of the codon number 380
 - (m) T/G polymorphism site for the third nucleotide of the codon number 497
 - (n) C/T polymorphism site for the third nucleotide of the codon number 453
 - (o) C/T polymorphism site for the third nucleotide of the codon number 478
 - (p) G/T polymorphism site for the third nucleotide of the codon number 507
 - (q) C/T polymorphism site for the third nucleotide of the codon number 1003 and
 - (r) G/C polymorphism site for the third nucleotide of the codon number 1120.
19. A method for evaluating the risk of suffering from cancer, which comprises analyzing LOH (Loss of Heterozygosity) in the genome region including KIAA0172 gene.
20. A method for evaluating the risk of suffering from cancer according to claim 19, which comprises determining loss of heterozygosity in either one or both of D9S1779 and D9S1858 which are microsatellite markers of chromosome 9p24 site.
21. A method for evaluating the risk of suffering from cancer, which comprises analyzing methylation of KIAA0172 gene.
22. The method for evaluating the risk of suffering from cancer according to claim 21, which comprises determining a methylation pattern of one or more CpG sequences present in KIAA0172 gene.
23. The method for evaluating the risk of suffering from cancer according to claim 22, in which the CpG sequence(s) is a CpG sequence(s) in the CpG island present in the 1st exon of KIAA0172 gene.